

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/520,258  
Source: PCT/10  
Date Processed by STIC: 1/13/05

***ENTERED***



PCT

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/520,258**

**DATE: 01/13/2005**  
**TIME: 17:15:06**

**Input Set : A:\20050-00003.ST25.txt**  
**Output Set: N:\CRF4\01132005\J520258.raw**

1 <110> APPLICANT: NEXGEN BIOTECHNOLOGIES, INC.  
 2 SHONG, Min-Ho  
 3 LEE, Sun  
 4 YOO, Jae-Geun  
 5 JIN, Seok-Min  
 7 <120> TITLE OF INVENTION: Production of Transformed Plants Expressing Thyroid Stimulating Hormone Receptor  
 10 <130> FILE REFERENCE: 20050-00003  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/520,258  
 C--> 12 <141> CURRENT FILING DATE: 2005-01-04  
 12 <150> PRIOR APPLICATION NUMBER: KR2002-38064  
 13 <151> PRIOR FILING DATE: 2002-07-02  
 15 <150> PRIOR APPLICATION NUMBER: PCT/KR2003/001308  
 16 <151> PRIOR FILING DATE: 2003-07-02  
 18 <160> NUMBER OF SEQ ID NOS: 2  
 20 <170> SOFTWARE: KopatentIn 1.71  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 2292  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (1)..(2289)  
 31 <400> SEQUENCE: 1  
 32 atg agg ccg gcg gac ttg ctg cag ctg gtg ctg ctg ctc gac ctg ccc 48  
 33 Met Arg Pro Ala Asp Leu Leu Gln Leu Val Leu Leu Leu Asp Leu Pro  
 34 1 5 10 15  
 36 agg gac ctg ggc gga atg ggg tgt tcg tct cca ccc tgc gag tgc cat 96  
 37 Arg Asp Leu Gly Gly Met Gly Cys Ser Ser Pro Pro Cys Glu Cys His  
 38 20 25 30  
 40 cag gag gag gac ttc aga gtc acc tgc aag gat att caa cgc atc ccc 144  
 41 Gln Glu Asp Phe Arg Val Thr Cys Lys Asp Ile Gln Arg Ile Pro  
 42 35 40 45  
 44 agc tta ccg ccc agt acg cag act ctg aag ctt att gag act cac ctg 192  
 45 Ser Leu Pro Pro Ser Thr Gln Thr Leu Lys Leu Ile Glu Thr His Leu  
 46 50 55 60  
 48 aga act att cca agt cat gca ttt tct aat ctg ccc aat att tcc aga 240  
 49 Arg Thr Ile Pro Ser His Ala Phe Ser Asn Leu Pro Asn Ile Ser Arg  
 50 65 70 75 80  
 52 atc tac gta tct ata gat gtg act ctg cag cag ctg gaa tca cac tcc 288  
 53 Ile Tyr Val Ser Ile Asp Val Thr Leu Gln Gln Leu Glu Ser His Ser  
 54 85 90 95  
 56 ttc tac aat ttg agt aaa gtg act cac ata gaa att cggt aat acc agg 336

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57 Phe Tyr Asn Leu Ser Lys Val Thr His Ile Glu Ile Arg Asn Thr Arg		
58 100 105 110		
60 aac tta act tac ata gac cct gat gcc ctc aaa gag ctc ccc ctc cta	384	
61 Asn Leu Thr Tyr Ile Asp Pro Asp Ala Leu Lys Glu Leu Pro Leu Leu		
62 115 120 125		
64 aag tcc ttg gca ttt tca aac act gga ctt aaa atg ttc cct gac ctg	432	
65 Lys Ser Leu Ala Phe Ser Asn Thr Gly Leu Lys Met Phe Pro Asp Leu		
66 130 135 140		
68 acc aaa gtt tat tcc act gat ata ttc ttt ata ctt gaa att aca gac	480	
69 Thr Lys Val Tyr Ser Thr Asp Ile Phe Ile Leu Glu Ile Thr Asp		
70 145 150 155 160		
72 aac cct tac atg acg tca atc cct gtg aat gct ttt cag gga cta tgc	528	
73 Asn Pro Tyr Met Thr Ser Ile Pro Val Asn Ala Phe Gln Gly Leu Cys		
74 165 170 175		
76 aat gaa acc ttg aca ctg aag ctg tac aac aat ggc ttt act tca gtc	576	
77 Asn Glu Thr Leu Thr Leu Lys Leu Tyr Asn Asn Gly Phe Thr Ser Val		
78 180 185 190		
80 caa gga tat gat ttc ttt ggg aca aag ctg gat gct gtt tac cta aac	624	
81 Gln Gly Tyr Asp Phe Phe Gly Thr Lys Leu Asp Ala Val Tyr Leu Asn		
82 195 200 205		
84 aag aat aaa tac ctg aca gtt att gac aaa gat gca ttt gga gga gta	672	
85 Lys Asn Lys Tyr Leu Thr Val Ile Asp Lys Asp Ala Phe Gly Gly Val		
86 210 215 220		
88 tac agt gga cca agc ttg ctg gac gtg tct caa acc agt gtc act gcc	720	
89 Tyr Ser Gly Pro Ser Leu Leu Asp Val Ser Gln Thr Ser Val Thr Ala		
90 225 230 235 240		
92 ctt cca tcc aaa ggc ctg gag cac ctg aag gaa ctg ata gca aga aac	768	
93 Leu Pro Ser Lys Gly Leu Glu His Leu Lys Glu Leu Ile Ala Arg Asn		
94 245 250 255		
96 agc tgg act ctt aag aaa ctt gca ctt tcc ttg agt ttc ctt cac ctc	816	
97 Ser Trp Thr Leu Lys Lys Leu Ala Leu Ser Leu Ser Phe Leu His Leu		
98 260 265 270		
100 aca cgg gct gac ctt tct tac cca agc cac tgc tgt gct ttt aag aat	864	
101 Thr Arg Ala Asp Leu Ser Tyr Pro Ser His Cys Cys Ala Phe Lys Asn		
102 275 280 285		
104 cag aag aaa atc aga gga atc ctt gag tcc ttg atg tgt aat gag agc	912	
105 Gln Lys Lys Ile Arg Gly Ile Leu Glu Ser Leu Met Cys Asn Glu Ser		
106 290 295 300		
108 agt atc gag acg ttg cgc cag aga aaa tct gtg aat gcc ttg aat agc	960	
109 Ser Ile Glu Thr Leu Arg Gln Arg Lys Ser Val Asn Ala Leu Asn Ser		
110 305 310 315 320		
112 ccc ctc cac cag gaa tat gaa gag aat ctg ggt gac agc att gtt ggg	1008	
113 Pro Leu His Gln Glu Tyr Glu Glu Asn Leu Gly Asp Ser Ile Val Gly		
114 325 330 335		
116 tac aag gaa aag tcc aag ttc cag gat act cat aac aac gct cat tat	1056	
117 Tyr Lys Glu Lys Ser Lys Phe Gln Asp Thr His Asn Asn Ala His Tyr		
118 340 345 350		
120 tac gtc ttc ttt gaa gaa caa gag gat gag atc att ggt ttt ggc cag	1104	
121 Tyr Val Phe Phe Glu Glu Gln Glu Asp Glu Ile Ile Gly Phe Gly Gln		

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122	355	360	365	
124	gag ctc aaa aac ccc cag gaa gag act cta caa gct ttt gac agc cat			1152
125	Glu Leu Lys Asn Pro Gln Glu Glu Thr Leu Gln Ala Phe Asp Ser His			
126	370	375	380	
128	tat gac tac acc ata tgt ggg gac agt gaa gac atg gtg tgt acc ccc			1200
129	Tyr Asp Tyr Thr Ile Cys Gly Asp Ser Glu Asp Met Val Cys Thr Pro			
130	385	390	395	400
132	aag tcc gat gag ttc aac ccg tgt gaa gac ata atg ggc tac aag ttc			1248
133	Lys Ser Asp Glu Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Lys Phe			
134	405	410	415	
136	ctg aga att gtg gtg tgg ttc gtt agt ctg ctg gct ctc ctg ggc aat			1296
137	Leu Arg Ile Val Val Trp Phe Val Ser Leu Leu Ala Leu Leu Gly Asn			
138	420	425	430	
140	gtc ttt gtc ctg ctt att ctc ctc acc agc cac tac aaa ctg aac gtc			1344
141	Val Phe Val Leu Leu Ile Leu Leu Thr Ser His Tyr Lys Leu Asn Val			
142	435	440	445	
144	ccc cgc ttt ctc atg tgc aac ctg gcc ttt gcg gat ttc tgc atg ggg			1392
145	Pro Arg Phe Leu Met Cys Asn Leu Ala Phe Ala Asp Phe Cys Met Gly			
146	450	455	460	
148	atg tac ctg ctc atc gcc tct gta gac ctc tac act cac tct gag			1440
149	Met Tyr Leu Leu Ile Ala Ser Val Asp Leu Tyr Thr His Ser Glu			
150	465	470	475	480
152	tac tac aac cat gcc atc gac tgg cag aca ggc cct ggg tgc aac acg			1488
153	Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Pro Gly Cys Asn Thr			
154	485	490	495	
156	gct ggt ttc ttc act gtc ttt gca agc gag tta tcg gtg tat acg ctg			1536
157	Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu			
158	500	505	510	
160	acg gtc atc acc ctg gag cgc tgg tat gcc atc acc ttc gcc atg gcc			1584
161	Thr Val Ile Thr Leu Glu Arg Trp Tyr Ala Ile Thr Phe Ala Met Ala			
162	515	520	525	
164	ctg gac cgg aag atc cgc ctc agg cac gca tgt gcc atc atg gtt ggg			1632
165	Leu Asp Arg Lys Ile Arg Leu Arg His Ala Cys Ala Ile Met Val Gly			
166	530	535	540	
168	ggc tgg gtt tgc ttc ctt ctc gcc ctg ctt cct ttg gtg gga ata			1680
169	Gly Trp Val Cys Cys Phe Leu Leu Ala Leu Leu Pro Leu Val Gly Ile			
170	545	550	555	560
172	agt agc tat gcc aaa gtc agt atc tgc ctg ccc atg gac acc gag acc			1728
173	Ser Ser Tyr Ala Lys Val Ser Ile Cys Leu Pro Met Asp Thr Glu Thr			
174	565	570	575	
176	cct ctt gct ctg gca tat att gtt ttt gtt ctg acg ctc aac ata gtt			1776
177	Pro Leu Ala Leu Ala Tyr Ile Val Phe Val Leu Thr Leu Asn Ile Val			
178	580	585	590	
180	gcc ttc gtc atc gtc tgc tgc tgt tat gtg aag atc tac atc aca gtc			1824
181	Ala Phe Val Ile Val Cys Cys Tyr Val Lys Ile Tyr Ile Thr Val			
182	595	600	605	
184	cga aat ccg cac aac cca ggg gac aaa gat acc aaa att gcc aag agg			1872
185	Arg Asn Pro His Asn Pro Gly Asp Lys Asp Thr Lys Ile Ala Lys Arg			
186	610	615	620	

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188 atg gct gtg atc ttc acc gac ttc acg tgc atg gcc cca atc tca	1920
189 Met Ala Val Leu Ile Phe Thr Asp Phe Thr Cys Met Ala Pro Ile Ser	
190 625 630 635 640	
192 ttc tat gct gtg tca gca att ctg aac aag cct ctc atc act gtt agc	1968
193 Phe Tyr Ala Val Ser Ala Ile Leu Asn Lys Pro Leu Ile Thr Val Ser	
194 645 650 655	
196 aac tcc aaa atc ttg ctg gta ctc ttc tat cca att aac tcc tgt gcc	2016
197 Asn Ser Lys Ile Leu Leu Val Leu Phe Tyr Pro Ile Asn Ser Cys Ala	
198 660 665 670	
200 aat cca ttc ctc tat gct att ttc acc aag gcc ttc cag agg gat gtg	2064
201 Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Ala Phe Gln Arg Asp Val	
202 675 680 685	
204 ttc atc cta ctc agc aag ttt ggc atc tgt aaa cgc cag gct cag gca	2112
205 Phe Ile Leu Leu Ser Lys Phe Gly Ile Cys Lys Arg Gln Ala Gln Ala	
206 690 695 700	
208 tac cgg ggg cag agg gtt cct cca aag aac agc act gat att cag gtt	2160
209 Tyr Arg Gly Gln Arg Val Pro Pro Lys Asn Ser Thr Asp Ile Gln Val	
210 705 710 715 720	
212 caa aag gtt acc cac gac atg agg cag ggt ctc cac aac atg gaa gat	2208
213 Gln Lys Val Thr His Asp Met Arg Gln Gly Leu His Asn Met Glu Asp	
214 725 730 735	
216 gtc tat gaa ctg att gaa aac tcc cat cta acc cca aag aag caa ggc	2256
217 Val Tyr Glu Leu Ile Glu Asn Ser His Leu Thr Pro Lys Lys Gln Gly	
218 740 745 750	
220 caa atc tca gaa gag tat atg caa acg gtt ttg t aa	2292
221 Gln Ile Ser Glu Glu Tyr Met Gln Thr Val Leu	
222 755 760	
225 <210> SEQ ID NO: 2	
226 <211> LENGTH: 763	
227 <212> TYPE: PRT	
228 <213> ORGANISM: Homo sapiens	
230 <400> SEQUENCE: 2	
231 Met Arg Pro Ala Asp Leu Leu Gln Leu Val Leu Leu Asp Leu Pro	
232 1 5 10 15	
234 Arg Asp Leu Gly Gly Met Gly Cys Ser Ser Pro Pro Cys Glu Cys His	
235 20 25 30	
237 Gln Glu Glu Asp Phe Arg Val Thr Cys Lys Asp Ile Gln Arg Ile Pro	
238 35 40 45	
240 Ser Leu Pro Pro Ser Thr Gln Thr Leu Lys Leu Ile Glu Thr His Leu	
241 50 55 60	
243 Arg Thr Ile Pro Ser His Ala Phe Ser Asn Leu Pro Asn Ile Ser Arg	
244 65 70 75 80	
246 Ile Tyr Val Ser Ile Asp Val Thr Leu Gln Gln Leu Glu Ser His Ser	
247 85 90 95	
249 Phe Tyr Asn Leu Ser Lys Val Thr His Ile Glu Ile Arg Asn Thr Arg	
250 100 105 110	
252 Asn Leu Thr Tyr Ile Asp Pro Asp Ala Leu Lys Glu Leu Pro Leu Leu	
253 115 120 125	
255 Lys Ser Leu Ala Phe Ser Asn Thr Gly Leu Lys Met Phe Pro Asp Leu	

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256	130	135	140	
258	Thr Lys Val Tyr Ser Thr Asp Ile Phe Phe Ile Leu Glu Ile Thr Asp			
259	145	150	155	
261	Asn Pro Tyr Met Thr Ser Ile Pro Val Asn Ala Phe Gln Gly Leu Cys		160	
262	165	170	175	
264	Asn Glu Thr Leu Thr Leu Lys Leu Tyr Asn Asn Gly Phe Thr Ser Val			
265	180	185	190	
267	Gln Gly Tyr Asp Phe Phe Gly Thr Lys Leu Asp Ala Val Tyr Leu Asn			
268	195	200	205	
270	Lys Asn Lys Tyr Leu Thr Val Ile Asp Lys Asp Ala Phe Gly Gly Val			
271	210	215	220	
273	Tyr Ser Gly Pro Ser Leu Leu Asp Val Ser Gln Thr Ser Val Thr Ala			
274	225	230	235	
276	240	Leu Pro Ser Lys Gly Leu Glu His Leu Lys Glu Leu Ile Ala Arg Asn		
277	245	250	255	
279	Ser Trp Thr Leu Lys Lys Leu Ala Leu Ser Leu Ser Phe Leu His Leu			
280	260	265	270	
282	Thr Arg Ala Asp Leu Ser Tyr Pro Ser His Cys Cys Ala Phe Lys Asn			
283	275	280	285	
285	Gln Lys Lys Ile Arg Gly Ile Leu Glu Ser Leu Met Cys Asn Glu Ser			
286	290	295	300	
288	Ser Ile Glu Thr Leu Arg Gln Arg Lys Ser Val Asn Ala Leu Asn Ser			
289	305	310	315	
291	320	Pro Leu His Gln Glu Tyr Glu Glu Asn Leu Gly Asp Ser Ile Val Gly		
292	325	330	335	
294	Tyr Lys Glu Lys Ser Lys Phe Gln Asp Thr His Asn Asn Ala His Tyr			
295	340	345	350	
297	Tyr Val Phe Phe Glu Glu Gln Glu Asp Glu Ile Ile Gly Phe Gly Gln			
298	355	360	365	
300	Glu Leu Lys Asn Pro Gln Glu Glu Thr Leu Gln Ala Phe Asp Ser His			
301	370	375	380	
303	Tyr Asp Tyr Thr Ile Cys Gly Asp Ser Glu Asp Met Val Cys Thr Pro			
304	385	390	395	
306	400	Lys Ser Asp Glu Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Lys Phe		
307	405	410	415	
309	420	425	430	Leu Arg Ile Val Val Trp Phe Val Ser Leu Leu Ala Leu Leu Gly Asn
310	430	435	440	
312	440	445	Val Phe Val Leu Leu Ile Leu Thr Ser His Tyr Lys Leu Asn Val	
313	450	455	460	
315	460	Pro Arg Phe Leu Met Cys Asn Leu Ala Phe Ala Asp Phe Cys Met Gly		
316	465	470	475	
318	480	Met Tyr Leu Leu Leu Ile Ala Ser Val Asp Leu Tyr Thr His Ser Glu		
319	485	490	495	
321	500	505	510	Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Pro Gly Cys Asn Thr
322	510	515	520	
324	520	525	Thr Val Ile Thr Leu Glu Arg Trp Tyr Ala Ile Thr Phe Ala Met Ala	

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/520,258

DATE: 01/13/2005

TIME: 17:15:07

Input Set : A:\20050-00003.ST25.txt

Output Set: N:\CRF4\01132005\J520258.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date